



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/501,962

DATE: 01/30/2005
TIME: 10:02:42

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\01302005\J501962.raw

```

3 <110> APPLICANT: Braun, Klaus
4      Braun, Isabell
5      Debus, Jurgen
6      Pipkorn, Rudiger
7      Waldeck, Waldemar
9 <120> TITLE OF INVENTION: CONJUGATE FOR TREATING PROKARYOTIC INFECTIONS
11 <130> FILE REFERENCE: 4121-170
13 <140> CURRENT APPLICATION NUMBER: 10/501,962
C--> 14 <141> CURRENT FILING DATE: 2004-07-19
16 <150> PRIOR APPLICATION NUMBER: PCT/DE03/00124
17 <151> PRIOR FILING DATE: 2003-01-17
19 <150> PRIOR APPLICATION NUMBER: DE 10201862.6
20 <151> PRIOR FILING DATE: 2002-01-18
22 <160> NUMBER OF SEQ ID NOS: 31
24 <170> SOFTWARE: PatentIn version 3.2
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 15
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Synthetic Construct
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35 attgttagat ttcat
38 <210> SEQ ID NO: 2
39 <211> LENGTH: 14
40 <212> TYPE: DNA
41 <213> ORGANISM: Artificial Sequence
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44 <223> OTHER INFORMATION: Synthetic Construct
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51 <211> LENGTH: 600
52 <212> TYPE: DNA
53 <213> ORGANISM: Artificial Sequence
55 <220> FEATURE:
56 <223> OTHER INFORMATION: Synthetic Construct
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61 ttgctaacgc agtcaggcac cgtgtatgaa atctaacaat gcgctcatcg tcattcctcg 120
63 caccgtcacc ctggatgtg taggcataagg cttgggtatg ccgggtactgc cgggcctt 180
65 gcgggatatac gtccatccg acagcatcgc cagtcactat ggcgtgctgc tagcgctata 240
67 tgcgttgatg caatttctat ggcacccgt tctcgagca ctgtccgacc gcttggccg 300

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Does Not Comply
 Corrected Diskette Needed
 (PG-S)

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69	ccgcccagtc	ctgctcgctt	cgctacttgg	agccactatac	gactacgcga	tcatggcgac	360									
71	cacaccggc	tcgtggatcc	tctacgccgg	acgcatacg	gccggcatca	ccggcgccac	420									
73	agg	tgcggtt	gctggcgct	atatcgccga	catcaccgat	gggaaagatc	480									
75	cttcgggctc	atgagcgctt	gtttcggcgt	gggtatggtg	gcaggccccg	tggccgggggg	540									
77	actgttggc	gccatctcct	tgcatgcacc	attccttgcg	gcggcggtgc	tcaacggcct	600									
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81	<211>	LENGTH:	109													
82	<212>	TYPE:	PRT													
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88	1				5					10					15	
91	Ser	Val	Ile	Gly	Gly	Ile	Gly	Thr	Phe	Leu	Met	Asp	Val	Arg	Asp	Gly
92						20				25					30	
95	Arg	Gln	Ser	Gly	Asn	Leu	Leu	Gly	Leu	Val	Thr	Glu	Ile	Phe	Val	Ala
96						35				40					45	
99	Val	Thr	Ala	Gly	Ala	Val	Ala	Tyr	Leu	Leu	Gly	Gln	His	Glu	Gly	Trp
100						50				55					60	
103	Glu	Leu	Ser	Ile	Thr	Tyr	Leu	Met	Val	Thr	Ile	Ala	Ser	Asn	Asn	Gly
104	65					65				70					75	80
107	His	Glu	Val	Ile	Ser	Gly	Met	Lys	Arg	Val	Asn	Ile	Asp	Ser	Ile	Leu
108							85				90					95
111	Asn	Val	Leu	Thr	Ser	Leu	Val	Lys	Lys	Gly	Gly	Gly	Lys			
112							100				105					
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116	<211>	LENGTH:	68													
117	<212>	TYPE:	PRT													
118	<213>	ORGANISM:	Bacteriophage H19B													
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123	1					5				10					15	
126	Thr	Gly	Tyr	Trp	Leu	Leu	Gln	Leu	Leu	Asp	Lys	Val	Ser	Pro	Ser	Gln
127						20				25					30	
130	Trp	Val	Ala	Ile	Gly	Val	Leu	Gly	Ser	Leu	Leu	Phe	Gly	Leu	Leu	Thr
131						35				40					45	
134	Tyr	Leu	Thr	Asn	Leu	Tyr	Phe	Lys	Ile	Arg	Glu	Asp	Arg	Arg	Lys	Ala
135						50				55					60	
138	Val	Arg	Gly	Glu												
139	65															
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143	<211>	LENGTH:	96													
144	<212>	TYPE:	PRT													
145	<213>	ORGANISM:	Bacteriophage A118													
147	<400>	SEQUENCE:	6													
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150	1					5				10					15	
153	Leu	Val	Val	Val	Thr	Pro	Val	Phe	Val	Gln	Ala	Ile	Lys	Lys	Thr	Glu
154						20				25					30	
157	Leu	Val	Pro	Ser	Lys	Trp	Leu	Pro	Thr	Val	Ser	Ile	Leu	Ile	Gly	Ala

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158	35	40	45	
161	Ile Leu Gly Ala Leu Ala Thr Phe Leu Asp Gly Ser Gly Ser Leu Ala			
162	50	55	60	
165	Thr Met Ile Trp Ala Gly Ala Leu Ala Gly Ala Gly Gly Thr Gly Leu			
166	65	70	75	80
169	Phe Glu Gln Phe Thr Asn Arg Ser Lys Lys Tyr Gly Glu Asp Asp Lys			
170	85	90	95	
173	<210> SEQ ID NO: 7			
174	<211> LENGTH: 143			
175	<212> TYPE: PRT			
176	<213> ORGANISM: Lactobacillus casei bacteriophage A2			
178	<400> SEQUENCE: 7			
180	Met Lys Ile Asn Trp Lys Val Ala Val Leu Ser Val Lys Phe Trp Leu			
181	1	5	10	15
184	Ala Leu Val Pro Ala Ala Leu Leu Val Val Gln Thr Ala Ala Ala Val			
185	20	25	30	
188	Phe Gly Tyr Asn Trp Asp Phe Ala Asn Leu Gly Lys Glu Leu Thr Ala			
189	35	40	45	
192	Val Ile Asn Ala Val Phe Ala Leu Leu Thr Ile Val Gly Val Ala Val			
193	50	55	60	
196	Asp Pro Thr Thr Glu Gly Val Ser Asp Ser Gln Gln Ala Leu Ala Tyr			
197	65	70	75	80
200	Pro Ala Leu Ile Thr Thr Lys Ala Ala Lys Ile Lys Ser Leu Glu Asp			
201	85	90	95	
204	Gln Ile Lys Ala Leu Gln Ala Asp Lys Ala Ala Asp Gln Ala Thr Ser			
205	100	105	110	
208	Ala Ala Ser Glu Val Val Pro Glu Thr Ser Ser Ala Ala Pro Ala Glu			
209	115	120	125	
212	Ser Ala Pro Glu Ser Val Ala Pro Val Ala Ser Glu Glu Val Lys			
213	130	135	140	
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217	<211> LENGTH: 142			
218	<212> TYPE: PRT			
219	<213> ORGANISM: Lactobacillus bacteriophage phig 1e			
221	<400> SEQUENCE: 8			
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224	1	5	10	15
227	Leu Ile Ser Phe Phe Ile Gly Val Ile Val Gln Ala Ile Lys Lys Thr			
228	20	25	30	
231	Gly Lys Val Lys Asn Thr Tyr Leu Pro Phe Ile Ser Met Gly Ile Gly			
232	35	40	45	
235	Ile Leu Ala Gly Leu Ala Ala Val Val Val Thr Lys Asp Thr Asn Tyr			
236	50	55	60	
239	Leu Asn Gly Ala Val Ala Gly Leu Ile Val Gly Ala Ala Thr Ser Gly			
240	65	70	75	80
243	Leu Thr Asp Gly Leu Ser Val Gly Thr Ser Ala Val Thr Thr Ala Lys			
244	85	90	95	
247	Ala Thr Lys Asp Ala Ala Lys Thr Ala Ala Ile Thr Gln Ala Val Leu			
248	100	105	110	

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251 Asn Ser Ile Asn Thr Thr Lys Ser Ser Asp Thr Thr Gln Val Ala Asn
252 115 120 125
255 Thr Ser Asn Thr Glu Gly Gly Ser Thr Ser Glu Thr Gln Lys
256 130 135 140
259 <210> SEQ ID NO: 9
260 <211> LENGTH: 107
261 <212> TYPE: PRT
262 <213> ORGANISM: Lactobacillus delbrueckii subsp. lactis bacteriophage LL-H
264 <400> SEQUENCE: 9
266 Met Thr Leu Ile Asp Trp Phe Asn Leu Ile Val Ala Ile Gly Thr Ile
267 1 5 10 15
270 Ala Leu Ala Val Val Ala Ser Val Tyr Val His Leu Lys Ala Lys Ile
271 20 25 30
274 Asp Thr Lys Thr Ala Ala Gly Lys Ala Phe Asp Leu Val Gly Lys Leu
275 35 40 45
278 Ala Val Trp Ala Val Asn Glu Ala Glu His Ser Gln Asp Gly Gly Ala
279 50 55 60
282 Ala Lys Arg Glu Phe Ala Ala Lys Leu Ile Ser Asp Gln Leu Lys Ala
283 65 70 75 80
286 Lys Gly Ile Thr Gly Ile Asp Glu Lys Met Val Tyr Gly Ala Val Glu
287 85 90 95
290 Thr Ala Trp Lys Glu Ala Ile Glu Asn Val Lys
291 100 105
294 <210> SEQ ID NO: 10
295 <211> LENGTH: 44
296 <212> TYPE: PRT
297 <213> ORGANISM: Lactococcus phage c2
299 <400> SEQUENCE: 10
301 Met Ile Glu Thr Leu Arg Ala Ile Gly Leu Val Val Phe Met Gln Leu
302 1 5 10 15
305 Leu Ser Leu Ala Leu Glu Phe Ile Asp Thr Gly Thr Leu Lys Pro Ser
306 20 25 30
309 Val Arg Lys Arg Ile Ala Val Glu Leu Met Val Leu
310 35 40
313 <210> SEQ ID NO: 11
314 <211> LENGTH: 74
315 <212> TYPE: PRT
316 <213> ORGANISM: bacteriophage phi AM2
318 <400> SEQUENCE: 11
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321 1 5 10 15
324 Thr Ala Leu Pro Ala Leu Ser Val Phe Ile Gly Val Ile Gly Lys Ala
325 20 25 30
328 Tyr Gly Trp Gly Gly Thr Asp Leu Ala Ile Ile Thr Leu Asn Ala Phe
329 35 40 45
332 Thr Val Phe Leu Gly Thr Leu Ala Gly Val Ser Ala Val Lys Tyr Asn
333 50 55 60
336 Ser Gln Pro Asn Asp Thr Lys Glu Asn Lys
337 65 70

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Input Set : A:\PTO.YF.txt
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340 <210> SEQ ID NO: 12
 341 <211> LENGTH: 88
 342 <212> TYPE: PRT
 343 <213> ORGANISM: Bacteriophage Tuc2009
 345 <400> SEQUENCE: 12
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 348 1 5 10 15
 351 Leu Ala Leu Leu Pro Ala Leu Phe Leu Leu Ile Gln Ala Ile Gly Ala
 352 20 25 30
 355 Pro Phe Gly Tyr Lys Trp Asp Phe Val Ile Leu Asn Gln Gln Leu Ala
 356 35 40 45
 359 Ala Val Val Asn Ala Ala Phe Ala Leu Leu Ala Ile Val Gly Val Val
 360 50 55 60
 363 Ala Asp Pro Thr Thr Ser Gly Leu Gly Asp Ser Asp Arg Val Leu Asn
 364 65 70 75 80
 367 Lys Asp Lys Ser Glu Glu Asn Lys
 368 85
 371 <210> SEQ ID NO: 13
 372 <211> LENGTH: 88
 373 <212> TYPE: PRT
 374 <213> ORGANISM: Bacteriophage TPW22
 376 <400> SEQUENCE: 13
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 379 1 5 10 15
 382 Leu Ala Leu Leu Pro Ala Leu Phe Leu Leu Ile Gln Ala Ile Gly Ala
 383 20 25 30
 386 Ser Phe Gly Tyr Lys Trp Asn Phe Val Ile Leu Asn Gln Gln Leu Ala
 387 35 40 45
 390 Ala Val Val Asn Ala Ala Phe Ala Leu Leu Ala Ile Val Gly Val Val
 391 50 55 60
 394 Ala Asp Pro Thr Thr Ser Gly Leu Gly Asp Ser Asp Arg Val Leu Asn
 395 65 70 75 80
 398 Lys Asp Lys Ser Glu Glu Asn Lys
 399 85
 402 <210> SEQ ID NO: 14
 403 <211> LENGTH: 74
 404 <212> TYPE: PRT
 405 <213> ORGANISM: homology to Orf78 of phage HP1 and gene S of phage P21
 407 <400> SEQUENCE: 14
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 410 1 5 10 15
 413 Gly Ser Ala Ile Ala Ile Tyr Ser Gly Phe Thr Leu Ala Asp Trp Ala
 414 20 25 30
 417 Ala Ile Phe Gly Ile Leu Phe Gly Leu Phe Thr Met Leu Ile Asn Trp
 418 35 40 45
 421 Tyr Tyr Lys Asn Lys Glu Ile Lys Leu Lys Glu Thr Ala Leu Lys Gln
 422 50 55 60
 425 Lys Ile Asp Leu Lys Glu Gly Asp His Glu
 426 65 70

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

PVS see item # 10 on error summary sheet

Invalid response

FYI: The above response can be inserted into section (2207)-(223).

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/501,962

DATE: 01/30/2005

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01302005\J501962.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date